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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          August 19, 2003, 09:30:20 ; Search time 8148 Seconds (without alignments) 11417.341 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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2274
                                      2888711 seqs, 20454813386 residues
                                                                                                                                                                                                                                                                                                                                                                                                 GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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gb_pat:*
gb_ph:*
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gb_htg:*
gb_in:*
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em_un:*
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em_vi:*
em_htg_inv:*
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gb_sy:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	o <sub>.</sub> o	000 00	Result NO. 1 1 2 2 3 6 6 7
545115387	304222200	10 111 111 111 111 111 111 111 111 111	987654W21
6006660066600066600066600666006660066600666006660066600666006660066600666006660066600666006660066600066600666006660066600666006660066600666000666006660006660006660006660006660006660006660006660006660006660006660006660006660000666000666000666000666000666000666000666000066600066600066600066600066600066600066600000666000666000666000066600066600006660000666000000	$\cdots \cdots $	75 6677 BBBB9 52 07	Score 2270.8 2270.8 756.4 720.8 664.4 664.4 438.4 215.8 180.2
		4.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6	Query Match 100.0 99.9 33.3 31.7 29.2 29.2 19.3 9.5
309 185730 255 110000 110000 110000 333321 719	9 225581 9 225581 9 110000 9 198550 9 326 8 32642 8 273275 8 273275	2066 2801 321 321 323 313 293650 145265 1348 110000 110000 203138 20029 25029 25029 25029 26021 262 282 282 282 282 282 282 282 282 282	Length 11289 , 2400 , 16207 10626 52900 311600 11420 2845 2263
		2253111311222121111	DB 1
AF009918 BX005453 AF009916 PEMAL13_24 PEMAL13_12 PEMAL13_13 AC115986 AY277502S3	BX510939 BX537105 BX005010_3 BX004991 AF009910 AF103869 AE014828 PFA929355	AGGU31115 AF009918 AF009913 AF009913 AP004172 AP004172 AF009920 AF009920 AF009926 BX530070 AF009915 AF009917 AF009917 AF009917 AF009917 AF009917 AF009911 AF009912 AF009912 AF009913 AF009913 AF009913 AF009913 AF009913 AF009913 AF009913 AF009913 AF009913 AF009913 AF009913 AF009913 AF009913 AF009913	ID AE006482 AB083107 AF447492 SPU49397 AE014138 AP005141 AP005141 STRERTNF SPSFB
AF009918 Streptoco BX005453 Danio rer AF009916 Streptoco Continuation (25 o Continuation (14 o AC116986 Dictyoste AY277504 Plasmodiu	105 105 105 991 910 869 828	1115 Group G 10990 Strept 109913 Strept 109913 Strept 109913 Strept 109920 Strept 109920 Strept 109915 Strept 109915 Strept 109917 Strept 109917 Strept 109917 Strept 109917 Strept 109917 Strept 109917 Strept 109918 Strept 109918 Strept 109918 Strept 109919 Strept 109918 Strept	Description AE006482 Streptoco AB083107 Streptoco AF447492 Streptoco U49397 Streptoco AE014138 Streptoco AP005141 Streptoco AB00963 Streptoco L10919 Streptoco C17947 S.pyogenes

## ALIGNMENTS

REFERENCE AUTHORS	SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION	DEFINITION	LOCUS	AE006482	RESULT 1
Streptococcus.  1 (bases 1 to 11289)  Ferretti.J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S.,	Streptococcus pyogenes M1 GAS Streptococcus pyogenes M1 GAS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	AE006482.1 GI:13621422	the complete genome. AE006482 AE004092	rain SF370, section	AE006482 11289 bp DNA linear BCT 01-JUN-2001		

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PUBMED
REFERENCE
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JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., | Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., Whyuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
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                                                                                                                                                                                                                                                                                                                                                       complement(3121. .3993)
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similar to Lactobacillus acidophilus dA/dG-kinase
(Streptococcus zooepidemicus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   City,
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kinase(I) subunit"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Streptococcus pyogenes M1 GAS'
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        CDS
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10519. .11166
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GQAPVQTEASIDQLYHFTLKDGESIKVTNLPVGVDYVVTEDDYKSEKYTTNVEVSPQD
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IPFVHHELTKGIAVAEISFDESILSIQELMYQVKEEKFQADLTKQLT"
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TNLFYSPYYKGNQKLYTSLKLIVEEMWAKLPGKRDLNHKHFHLECHTYEEQSLRNIQPP
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                                                                                                                       KLKINIFACIQTDAFDSLLFNPIDVDISSKNEFLNHIKQKSVQYREILTTNESRFVAL
                                                                                                                                                     SGSVFLDYRNKVTFEDKYSLIYAHHMAGNVMFGELPNFRKKSFFNKHKEFSIETKTKQ
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                                                                                                                                                                                                                                                                                                                                                                           /note="Best Blastp hit = gb|AAC97152.1| (U49397) unknown
|Streptococcus pyogenes]"
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(Streptococcus pyogenes]"
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|Streptococcus pyogenes]"
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/protein_id="nak33240.1"
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/note="Best Blastp hit = gb|AAC97151.1|
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                                                                                                                                                                                                                                                              Submitted (03-APR-2002) Tohru Miyoshi-Akiyama, Tokyo Women's Medical University, Department of Microbiology and Immunology; Kawada-cho, Shinjuku-ku, Tokyo 162-8666, Japan (E-mail:KFA01112@nifty.ne.jp, Tel:81-3-3353-8111(ex.22713), Fax:81-3-5269-7411)
                                                                                                                                                                                                                                                                                                                               Miyoshi-Akiyama, T., Wakisaka, N.,
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TPGDPPMPPNOPOTTSVLIRKYAIGDYSKLLEGATLOLTGDWNSFOARVESSNDIGE
RIELSDCTYTLTELNSPAGYS LAEPITFKVEAGKVYTILDGKQIENPNKETVEPYSVE
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FEIELKNNKQELLSQTVKTDXTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETD ISLGIWGIHTIRIRKHD" 364 c 463 g SEGYKVKVNSQEVANATVSKTGITSDETLAFENNKEPVVPTGVDQKINGYLALIVIAG g 700

Query Match Best Local Similarity Matches 2272; Conserv GGATACCAAAATCTTTTGAGTGGTGGTTTAGTTCCTACTAAACCACCAACTCCAGGAGAC GGGCATCCATATTATAAACAGTTTAGAGTAGCACACGATTTAAAGGGTTAACTTAGAAGGA GCAATAAATCCAGATTCAAGTTCGGAATACAGATGGTATGGATATGAATCTTATGTAAGA GTAACTTCCATGGTTGGTGCTAAGACTGTTTTTGGTTTAGTAGAATCCTCGACGCCAAAC AAAAACTCAAAACGATTTACTGTCACTTTAGTGGGAGTCTTTTTAATGATCTTCGCTTTG ATGAAAAAAACAAGGTTTCCAAATAAGCTTAATACTCTTAATACTCAAAGGGTATTAAGT GAAAGTTTTAAAAGGGAGTCAGAAAGTAACTTGGTTAGTACTTCTCAATTATCTTTGATG AGAGTTACACAAGAGGCGGTATGGTACTATTCTGATAATGCTCCTATTTCTAATCCAGAT AATGGACATCCACAAAATGCCAATGGTATTATGGAAGGCTTGGAACCCTTGAATGCTATC GCGATGAGCCCTAGAATTACGGGAGATGAGCTAAATCAGAAGTTACGAGCTGTTATGTAT 480 GTAACTTCCATGGTTGGTGCTAAGACTGTTTTTGGTTTAGTAGAATCCTCGACGCCAAAC CGTCAAGCTTTGAAGCAACTGATTGATCCGAATTTGGCAACTAAAATGCCAAAACAAGTT AATGGACATCCACAAAATGCCAATGGTATTATGGAAGGCTTGGAACCCTTGAATGCTATC GCGATAAGCCCTAGAATTACGGGAGATGAGCTAAATCAGAAGTTACGAGCTGTTATGTAT AGTAGTGTTAAAAAGTGGTATAAAAAAACATGATGGAATCTCTACAAAATTTGAAGATTAT AGTAGTGTTAAAAAGTGGTATAAAAAAACATGATGGAATCTCTACAAAATTTGAAGATTAT GCAATAAATCCAGATTCAAGTTCGGAATACAGATGGTATGGATATGAATCTTATGTAAGA AGAGTTACACAAGAGGCGGTATGGTACTATTCTGATAATGCTCCTATTTCTAATCCAGAT Conservative 99.98; 0; Score 2270.8; Pred. No. 0; 0; Mismatches DВ 2 ۲. Indels Length 0; Gaps 153 840 873 780 720 600 540 573 513 420 453 360 393 300 240 180 60 813 753 660 693 633 333 273 213

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Bessen, D.E. and Kalia, A. Genomic localization of a T serotype lo zone encoding extracellular matrix-bind Streptcoccus pyogenes
Infect Immun. 70 (3), 1159-1167 (2002)
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Bessen, D.E. and Kalia, A.
Direct Submission
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Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Oy Db	0y 0y 0y	Qy Db	O	Q D Qy	Оу	Qу	Qy Db	Qy	Оу	Qy Db	Qу	Оу	Qy Db	ФФ
70 05 30 65 90	1788 AAAAGAAGTTATACCTGTAACTCATAATTTAACATTGAGAAAAACGGTGACTGGTTT 1844	90 TAGTGCCCCTCAACTAACAATCTTGATTTCTTCGTACTAATAATAGCAAATACCAATC 28 TCTTATTGGAACTCAGTGGCATCCAGAAGATTTAGTTGATATTATTCGTATGGAAGATAA 28 TCTTATTGGAACTCAGTGCCAGAAGATTTAGTTGATATTATTCGTATGGAAGATAA 30		1500 TGGTCTAACTGAGACACAATTGCGTGCGGCTACTCAGTTAGCAATATATTATTTCACTGA 1559	1440 ACATATCAAAAAAGTAATTGAGAAGGGTTACAGGGAAAAAGGACAAGCTATTGAGTATAG 1499 	1380 TCGTGACCTCTTTAAATATACTGTGAAACCAAGAGATACCGATCCTGACACTTTCTTAAA 1439	1323 GAAAACAATGACTCCAGACTTTACAACAGGAGAAGTAAAATACACTCATATTGCAGG 1379	1263 ACAGGTTGTCTATTGCTTTAATGCAGATCTAAAATCTCCACCAGACTCTGAAGATGGTGG 1322 	1212 TACACAAAACTATGCAAAATTTTATTATGCAAAAAATAAAAATGGAAGTTC 1262 	1152 GATAGTAGAGCCTTACTCAGTAGAAGCATATAATGATTTTGAAGAATTTAGCGTTTTAAC 1211	1095 AGCTGGCAAAGTGTATACTATTATTGATGGAAAACAGATTGAAAATCCCAATAAÁGA 1151	35 AACTGAATTGAATTCTCCAGCTGGTATAGTATCGCAGAGCCAATCACTTTAAGGTTGA	75 AGTGTTTAGCAGTAATGATATTGGAGAAAGAATTGAACTATCAGATGGAACTTATACTTT	6216 ACTTCTAGAGGGAGCAACTTTGCGTTTAACAGGGGAAGATATCCTAGATTTTCAAGAAAA 6275

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RESULT 4
SPU49397/c
LOCUS
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REFERENCE
AUTHORS
TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                      CDS
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                                                                                                                                                                                                                                                                                                                                     gene
                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LUBZO DP DNA linear BCT 19-DEC-Streptococcus pyogenes MsmR (msmR) gene, partial cds; LepA (lep Cpa (cpa), and Nra (nra) genes, complete cds; SsbA (ssbA) gene, partial cds; and unknown genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-FEB-1996) RWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiology,
Germany, 52074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Podbielski, A., Woischnik, M., Leonard, B.A.B. Characterization of nra, a global negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U49397.1 GI:4028947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Podbielski, A. and Woischnik, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATGACT 2272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTATTGCTTGTCCCATTTGGTTTGTTAGTGTGGTTCTTTGGTCGTAAAAGGACTAAAAAA 7589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATAGTTATCGCTGGTATCAGTTTGGGGATCTGGGGAATTCACACGATAAGGATAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGTAAAGATCTTGTCCCCACCAACTGGTTTTATTACTGATGGTGGAACCTATCTGTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAATAAAGAGCCTGTTGTTCCTACAGGAGTTGATCAAAAGATCAATGGCTATCTAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAAGAAGCTCAATCAGCAAGTGAGAATGTCACAGCAGACAAAGAAGTCACTTTTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCAAATGCTACAGTTTCAAAAACAGGAATAACAAGTGATGAGACACTTGCTTTTGAAAA 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 10826)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiol. 31 (1999) In press
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pyogenes
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                                      .1377)
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                                                                                                                                                                                                                                                                                                                                                                                                      pyogenes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               negative regulator gene
                                                                     terminator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmidt, K.H.
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s; LepA (lepA),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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                                                                                                     -10_signal
                                                  35_signal
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KGKISTLLRVRGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPSYTDDNVLMPKADYSFKVEADDNAKGKTKDGLDIKPGVIDGLENTKTIRYSNSDKI
TAKEKSVNFEBANVKFPGVGVRYTVAEVNGNAKGITTVDSQXPTVDVYVVNKEGGGFE
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complement(5972.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,....e="ORF 4; similar to peptidase 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to electron transfer flavorprotein 1 of Methylophilus electron; ORF 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLPLAGEVKSLLGILSIVLLGLLVLLYVKKLKSRL"
                                                   EAQSVGKDITEDKKVTFENRKDLVPPTGLTTDGAIYLWLLLLVPLGLLVWLFGRKGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3705. .5933)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="lepA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3191. .3712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KFVAFSTCENFSTDNRVIVVGTIQE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KERKKLTVTIFACLKTDAFDQLVFNPNAITNQDQQRQLVDYISKRSKQFKPVKLKHHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="cpa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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.6102)

.6148)

180

5776

120

5835

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SQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note='
                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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8024. .8857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="extended promoter
complement(6161. .6166)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPDLVITHSRLIPFVKNDLVKGVTVAEFSFDKPDYSIASIQNLIYQLKDKKYQDFLNE
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                                      CCACCAATGCCTCCAAATCAACCTCAAACGACTTCAGTACTTATTAGAAAGTATGCTATA
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                                                                              GGTGATTACTCTAAATTGCTTGAAGGTGCAACATTACAGTTGACAGGGGATAACGTGAAT
                                                                                                                                                          ----AGAGCCTCCGGCTAAAACTGAAAAAACATCAGTCATTATCAGAAAATATGCGGAA
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                                                                                 GGGAAATATTCATTTAATCTAAAGCATGGTGACACCATAAGAATAGAAGGATTACCGACG
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JOURNAL
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Beres, S.B., Sylva, G.L., Barbian, K.D., Lei, B., Hoff, J.S., Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F., Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M.
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Beres,S.B., Sylva,G.L., Barbian,K.D., Lei,B., Hoff,J.S.,

Mammarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,

Markins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes MGAS315
Streptococcus pyogenes MGAS315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-JUN-2002) Laboratory of Human-Bacterial Pathogenesis, Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St., Hamilton, MT 59840, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Musser, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phage-encoded toxins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Musser, J.M. Genome sequence of a serotype M3 strain of group A Streptococcus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome.
AE014138 AE014074
AE014138.1 GI:21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTGGTTGTTATTACTTGTTCCACTTGGGTTATTGGTTTTGGCTATTTGGTCGTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTAGCTTTGATAGTTATCGCTGGTATCAGTTTGGGGGATCTGGGGAATTCACACGATAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A.
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QVISIEDPVEIKNHQILQLQVNDDIGMTYDNLIKLSLRHRPDILVIGEIRDSQTARAV
                                                                                                                                                                                                                                                                                                           gordonii]"
                                                                                                                                                                                                                                                                                                                              putative ABC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Streptococcus
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/strain="MGAS315"
                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="comYA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:198466"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /serotype="M3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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MGAS315,
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of 37 of
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the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /2273. 2/10
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2273. .716
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KVECHLFFSHFEHLYRHQOKLAILQQKQRVLDISSTKIVTEGNSLTVPKSITVNHPYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative competence protein"
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/note="best non-GAS blastp hit:
(AE006440) hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SpyM3_0082"
2673. .2957
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GTLIGQGLDLMTILDIMAIEKSSLMKELAEDIRMSLLEGQAFHIKVATYPFFKKELSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIAFLKRSQLLQLDYVLKMEESLLKGQGLADMLSGLGFSDAILTQISLADRHGNIETT
LVAIQHYLNQMARIRRKTVEVITYPLILLLFLFVMMLGLRRYLVPQLETQNQITYFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative ABC /protein_id="AAM78686.1 /db_xref="GI:21903797"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="best non-GAS blastp hit: gb|AAC45311.1| (U81957)
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                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
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ComYC [Streptococcus gordonii]"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="comYC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="comYB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="synonym: SpyM3_0079"
                                                                                                                                               note="synonym: Spym3_0083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SpyM3_0080*
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[Lactococcus lactis subsp.
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PIPQKYYTDYKYRKYGAHGTSHKYVAQEAKHLGRPLEEKLITAHTGUNGVSJTANV
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/gene="SpyM3_0087"
6186. .6494
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3792. .4745
/gene="SpyM3_0085"
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hypothetical protein [Streptococcus pyogenes M1 G
/codon_start=1
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/codon_start=1
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/db_xref="GI:21903805"
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kinase (Streptococcus pyogenes MI GAS]"
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EQLSDKDSLEVLEIGSGTGNLAQTLLNNTSKSLDYVGIELDDLLIDLSASIAEIMDSS
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/protein_id="AAM78692.1"
/db_xref="GI:21903803"
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hypothetical protein [Streptococcus
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/protein_id="AAM78690...
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/note="best blastp
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901 GGTGATTACTCTAAATTGCTTGAAGGTGCAACATTACAGTTGACAGGGGATAACGTGAAT	781 GGATACCAAAATCTTTTGAGTGGTGGTTTAGTTCCTACTACACCACCACCTCCAGGAGAC	661 CGTCAAGCTTTGAAGCAACTGATTGATCGAATTTGGCAACTAAAATGCCAAAACAAGTT	541 AGAGTTACACAAGAAGCGGTATGGTACTATTCTGATAATGCTCCTATTTCTAATCCAGAT	421 GCGATGAGCCCTAGAATTACGGGAGATGAGCTAAATCAGAAGTTACGAGCTGTTATGTAT	301 AGTAGAAGTTATCAAGTTTATTGCTTTAATTTAAAGAAAG	181 GCAATAAATCCAGATTCAAGTTCGGAATACAGATGGTATGGATATGAATCTTATGTAAGA  15722TAAACAAAGCTCAGTTCAAGATTATCCGTATGGCTATGGTATGATTCTTATTCTAAA  241 GGCATCCATATTATAAACATTTAGAGTTAGCACACGATTTAAGGTTAGATGTAGAAGAAGA  241 GGCATCCATATTATAAACAGTTTAGAGTTAGCACACGATTTAAAATTTAAAATTTAGATGGA  1	Match 29.2%; Score 664.4; DB 1; Length 52900; Local Similarity 60.0%; Pred. No. 2.1e-103; les 1318; Conservative 0; Mismatches 816; Indels 64; Gaps 61 AAAAACTCAAAACGATTTACTGTCACTTTAGTGGGAGTCTTTTTAATGATCTTCGCTTTG 61
960 Db 1 16472 Qy 1020 Db 1 16532 Qy 1080 Db 1 16592 Qy	840	720 Oy 16256 Db 780 Db 16298 Db	600 Qy 16136 Db 1 660 Qy 16196 Db 1	480 OY 16016 Db 1 540 OY 16076 Db 1	360 Qy 15896 Db 12896 Qy 420 Db	240 Db 15776 Qy 300 Db	10; Db 120 Dy 15662 Db 15721 Db
	1037 ACTGGATIAGCIGGEGAAAGTATAAAAATICAATITAAAATACAGTTTAAAATTACAGATAAAATACATTTAAAATTCTTCT 117367 ACTGGAACTATTGCAGATAAGAAAAAAAAAAATTTAAAAATACATTTAAAATTCTTCT 1897 AAGCAAGAATTGCTTTCTCAAACTGTTAAAACAGATAAAACAAAACCTCGAATTTAAAAGT 1897 AAGCAAGAATTGCTTTCTCAAACTGTTAAAAACAGATAAAAACAAAC		1600 GGTTTTGGAGACATGAATAGTAGTTTGAGCAGTTGCTAAAATCCTTGTAGAATACGCT	1492 GAGTATAGTGGTCTAACTEGAGCACAATTGCGTGGGTGACTCAGTTAGCAATATATTAT	1372 ATTGCAGGTCGTGACCTCTTTAAATATACTGTGAAACCAAGATACCGATCCTGACACT	16773 GGAACTAATCAAGTTGTCTACTGTTTCAATGCTGATTTACACTCACCACCTCACTCA	1001 CITTIANOSTI CHOCATONOST CONTROL C

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Streptococcus pyogenes SSI-1
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Streptcoccus pyogenes SSI-1 DNA,
APO05141 BA000034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Sequence of an M3 Strain of Streptococcus pyogenes Reveals
Large-Scale Genomic Rearrangement in Invasive Strains and New
Insights into Phage Evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakagawa,I., Kurokawa,K., Yamashita,A., Nakata,M., Tomiyasu,Y., Okahashi,N., Kawabata,S., Yamazaki,K., Shiba,T., Yasunaga,T., Hayashi,H., Hattori,M. and Hamada,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Japan (E-mail:ken@gen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-MAY-2002) Ken Kurokawa, Osaka University, Information Research Center; 3-1, Yamadaoka, Suita, Osak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamashita,A., Nakagawa,I., Kurokawa,K., Nakata,M., Tomiyasu,Y.,
Yamazaki,K., Okahashi,N., Kawabata,S., Yasunaga,T., Hattori,M.,
Hayashi,H. and Hamada,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AP005141.1 GI:28810157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               like syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2683278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone was isolated from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Res. 13 (6),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1042-1055 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patient presenting with toxic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pyogenes SSI-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SPs0005"
4665. .5234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4665
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/note="similar to GB:AAK33149.1 (AE006472) percent

identity 98 in 371 aa"
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3480. .4595
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QVVLTSGKSEITLKGKDVDQYPRLQEVSTENPLILKTKLLKSIIAETAFAASLQESRP
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LTRAAYHLLGLGTYFTAGEKEVRAWTFKRGIKAPQAAGIIHSDFERGFIRAVTMSYDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3480.
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identity 100 in 65 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dentity 99 in 378 aa
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.1"
                                                                                                                                                       (AE006472) percent
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Query Match
Best Local S
Matches 1318
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                                                                                                                    1318;
                                                                                                                                         Similarity
                                               AAAAACTCAAAAACGATTTACTGTCACTTTAGTGGGAGTCTTTTTAATGATCTTCGCTTTG 120
                       AACAAACGACGACAAACGACGATCGGATTACTGAAAGTATTTTTGACGTTTGTAGCTCTG 111843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADMESMOPMDRLLVGDVGFGKTEVAMRĀĀFKAVNDHKQVĀVLVPTTVLĀQQHYENFKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YQKVSQVISPGEFSRRGDILDIYEITQELPYRLEFFGDDIDSIRQFHPETQKSFEQLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQSGFIDSVGFEMYSQLLEQAIASKQGKTTVRQKGNTEINLQIDAYLPDDYIADERQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDDQKKIVVVTSTQNEVEKLASDLSSLLDEELVFQFFADDVAAAEFIFASMDKALSRI
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                                                                                                                                                                                                                                                                                                                                                                                           /gėne="SPs0009"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAC63103.
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60.0%;
                                                                                                               Score 664.4; DB 1;
Pred. No. 1.3e-103;
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                                                                                                                                                                               ACTITIAAGGIIGAAGCIGGCAAAGIGI----AIACIATIAIIGAIGGAAAACAGAIIGAA 1137
                                                                                                                                                                                                                                                                                                                         GGTTTTCAGGAGAAAATTTTTGATAGTAACAAGTCTGGAGAGAAAGTAGAGCTACCTAAT
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TTTAGCGTTTTAAC - - - TACACAAAACTATGCAAAATTTTATTATGCAAAAAATAAAAAAT
                                             AACCAAAATAAGGAAATCGCAGAGCCATATTCTGTAACAGCTTTCAATGACTTTGAAGAG
                                                                                       AATCCCAATAAAGAGATAGTAGAGCCTTACTCAGTAGAAGCATATAATGATTTTGAAGAA 1197
                                                                                                                                    ACTTTTAAAGTTGCAGCTGAGAAAGTTTTAATAAAAAATAAAGAAGGTCAATTTGTAGAG 112833
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22 tp		RESULT 7	_
/gene="spyM18_0122" complement(1418 2395)	CDS	Db 113904 CTATCTTTGGTTGTTATTACTTGTTCCATTTGGGTTAT 113941	_
I KUSILIANNILEELEGMEANKPULLI I LUVSEURMLEK IERKISKSE EQVUUNESLEQI I HQVQHQEKPTWYEDYKVSPKMKIDGNSLDEVQNPQDLATVLKMIDTKLKELHLL" COmplement (1418 2395)	gene		_
/brotell_id= naisoss.i /db_xref="GI:19747396" /translation="MLIVLAGTIGAGKSSLAAALGEHLGTDVFYEAVDNNPVLDLYYQ DPKKYAFILQIYFLNKRFKSIKEAYQADNNILDASIFEDELFLKLNYKNGNYTKTELD		Qy 2137 TITGAAAATAAAGAGCCTGTTGTTCCTACAGGAGTTGATCAAAAGATCAAATGGCTAT 2196	
/codon_start=1 /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein id="hn16692" 1"		OY 2077 CAAGAAGTAGCAAATGCTACAGTTTCAAAAACAGGAATAACAAGTGATGAGACACTTGCT 2136	
complement(7571398) /gene="spyM18_0121" /note="best blastp match gb AAC97156.1  (U49397) unknown [strentococcus mooreneel"	CDS	Qy 2017 GGTTATTCTTACCTTGTCAAAGAAACAGATTCTGAAGGCTATAAGGTTAAAGTTAATAGC 2076	
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/transl_care=11 /product="putative single-strand binding protein" /protein_id="AAL96931.1" /protein_id="AAL96931.1" //tapall-tide="MAL96931.5"		OY 1897 AAGCAAGAATTGCTTTCTCAAACTGTTAAAACAGATAAAACAAAC	
(ARD06276) single-strand binding protein [Lactococcus lactis subsp. lactis]"  /cocon_start=1		Qy 1837 ACTGGTTTAGCTGGTGACAGAACTAAAGATTTCCATTTTGAAATTGAAATTAAAAAATAAT 1896	
/gene="seb" /note="gynonym: spyM18_0120" 107502 /gene="ssb"	CDS	QY 1780 GAAGATAAAAAAGAAGTTATACCTGTAACTCATAATTTAACATTGAGAAAAAGGGTG 1836	
/#ULL-LFE 9500012 DVA /strain="MGAS823" /db_xref="taxon:186103" 107502 /mone_Tsch"	gene	OY 1720 TATCAATCTCTTATTGGAACTCAGTGGCATCCAGAAGATTTAGTTGATATTATTCGTATG 1779	
	FEATURES Source	OY 1660 CAAGATAGTAATCCTCCACAGCTAACTGACCTTGATTTCTTATTCCGAATAACAATAAA 1719	
Direct Submission  Direct Submission  Submitted (31-JAN-2002) Laboratory of Human Bacterial  Pathogenesis/Rocky Mountain Laboratories/NIAID/NIH, 903 S. 4th St.,  Hamilton wr 50840 Ura	TITLE JOURNAL	Qy 1600 GGTTTTGGAGACATGAATGATAGTACTTTAGCAGTTGCTAAAATCCTTGTAGAATACGCT 1659	
<pre>2 (bases 1 to 11420) Smoot.J.C., Barbian,K.D., Van Gompel,J.J., Smoot,L.M., Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M., Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M., Zhang,Q., Kapur,V., Dalv.I.A., Veasy,L.George and Musser.I.M.</pre>	AUTHORS	OY 1552 TTCACTGATAGTGCTGAATTAGATAAGGATAAACTA	
	JOURNAL MEDLINE PUBMED	OY 1492 GAGTATAGTGGTCTAACTGAGACACAATTGCGTGCGGCTACTCAGTTAGCAATATATTAT 1551	
Porcella, S.F., Parkins, L.D., Beres, S.B., Campbell, D.S., Smith, T.M., Zhang, Q., Kapur, V., Daly, J.A., Veasy, L.G. and Musser, J.M. Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks.	TITLE	OY 1432 TTCTTAAAACATATCAAAAAAGTAATTGAGAAGGGTTACAGGGAAAAAGGACAAGCTATT 1491	<b>"</b> ~
1 (bases 1 to 11420) 1 (bases 1 to 11420) Smoot, J.C., Barbian, K.D., Van Gompel, J.J., Smoot, L.M., Chaussee, M.S., Sylva, G.L., Sturdevant, D.E., Ricklefs, S.M.,	REFERENCE AUTHORS	OY 1372 ATTGCAGGTCGTGACCTCTTTAAATATACTGTGAAACCAAGAGATACCGATCCTGACACT 1431	п -
Streptococcus pyogenes MGAS8232 Streptococcus pyogenes MGAS8232 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	SOURCE ORGANISM	OY 1315 GATGGTGGGAAAACAATGACTCCAGACTTTACAACAGGAGAAGTAAAATACACTCAT 1371 Db 113014 GATCACGGAGCAAATATTGATCCTGATGTCAGTGAAAGTAAAAGAGATAAAAGTATACACAT 113073	
Streptococcus pyogenes strain MGAS8232, section 11 of 173 of the complete genome. AE009963 AE009949 AE009963.1 GI:19747394	DEFINITION ACCESSION VERSION	OY 1255 GGAAGTTCACAGGTTGTCTATTGCTTTAATGCAGATCTAAAAATCTCCACCAGCTCTGAA 1314	
	AE009963	Db 112894 ATTGGTTATTTATCTGATTTTAATAACTATGGTAAGTTTTACTATGCAAAAAATACTAAT 112953	_

gene

CDS

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misc_feature
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                                                                                                                                                                                                                                                                 GAEEQSTETKKTSV11RKYAEGDYSKLLEGATLKLAQ1EGSGF0EQSFESSTSG0KLQ
LSDGTY1LTETKSPQGYE1AEP1TFKVTAGKVF1KGKDGQFVENQNKEVAEPYSVTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="cbp"
/note="best blastp match gb|AAC97148.1| (U49397) Cpa
[Streptococcus pyogenes]"
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TLIANQILAANQKGDSKITVKVIGDSSFGHIISVADTKGHVKGYIQNTGVDIKKTATG
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LLDENDKVKVAGGFMVQVLPGASEEEIARYEKRLQEMPAISHLLASKNHVDALLEAIY
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                                                                                         ASDYEVSVNGKNAPDGKATKASVKEDETITFENRKDLVPPTGLTTDGAIYLWLLLLVI
                                                                                                                  VPNSNKYQSLIGTQYHPESLVDIIRMEDKQAPIIPITHKLTISKTVTGTIADKKKEFN
FEIHLKSSDGQAISGTYPTNSGELTVTDGKATFTLKDGESLIVEGLPSGYSYEITETG
                                                                                                                                                                                EGKEIKYTHILGADLFSYANNPRASTNDELLSQVKKVLEKGYRDDSTTYANLTSVEFR
AATQLAIYYFTDSVDLDNLADYHGFGALTTEALNATKEIVAYAEDRANLPNISNLDFY
                                                                                                                                                                                                                                           NDFDDSGFINPKTFTPYGKFYYAKNANGTSQVVYCFNVDLHSPPDSLDKGETIDPDFN
                                                                                                                                                                                                                                                                                                                            /product="putative collagen binding protein"
/protein_id="AAL96936.1"
/db.xref="G1:19747400"
/translation="MQKRDKTNYGSANNKRRQTTIGLLKVFLTFVALIGIVGFSIRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5345.
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RYLIAMLYSKFGIVIYPLDHLDNQIIYRFLSQSATNLRTSPWLEEPFSFYNMLLALS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTGLTAVQLKYYCKELDDFFGNNLDITIKKGKIICCFVKPVKEFYLHQLYDTSTILKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="N-terminal fragment of Nra"
/protein_id="AAL96935.1"
/db_xref="GI:19747399"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="synonym: spyM18_0125"
complement(4262. .4915)
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/gene="nra.1"
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/protein_id="AAL96934.1"
/db_xref="GI:19747398"
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complement/
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LKGETIAVREFRGLAPHYLAGTAGAAKVRGAVSRAETLAEVEAIFETVR"
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DINMGCPVNKYVKNEAGAKWLRDPDKIYHIVKEVTSVLDIPLTVKMRTGWADSSLAVE
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/protein_id="AAL96933.1"
/db_xref="GI:19747397"
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[Streptococcus pyogenes]"
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1034 TAACTGAATTGAATTCTCCAGCTGGTTATAGTATCGCAGAGCCAATCACTTTTAAGGTTG 1093
                                                                                                                                                                                                                                       5493
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                                                                                                                                                                                                                                                          854 CAAATCAACCTCAAACGACTTCAGTACTTATTAGAAAGTATGCTATAGGTGATTACTCTA 913
                                                                                                                                                                                                                                                                                                                                 863;
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                                         AGAGTTTTGAAAGTACTTCAGGACAAAAATTGCAGTTGTCGGATGGTACATATTT
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                                                                                            GAGTGTTTAGCAGTAATGATATTGGAGAAAGAATTGAACTATCAGATGGAACTTATACTT 1033
                                                                                                                                        Conservative
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9246. .
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8489. .9229
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VDGSVAMSGSLFLDYBRHNDEYDDYSLIYGHHMAGNAMFBEIPKFLKKAF
VDGSVAMSGSLFLDYBRHNDEYDDYSLIYGHHMAGNAMFBIPKFLKKEFKKLFVKLK
IETKERKKLTVTIFACLKTDAFDQLVFNPNAITNQDQQRQLVDYISKRSKQFKPVKLK
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TAKEKSYNFDFANYKFPGVGYTRYTVSEVNGNKAGIAKDGXDGYTDVYVNNTEDGGFE
AKYLYSTEGGOSDKKEVLFKNFFDTYSLKYTKKKYTGNTGEHORSFSFTLLTPNECFE
KGQVVNILQGGETKKVVIGEEYSFTLKDKESVTLSQLPVGIEYKVTEEDVTKDGYKTS
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/protein_id="AAL96937.1"
/dzyref="G1:19747401"
/tzanslation="MINYLNRLNENPLFKAFIRLVLKISIIGFLGYILFQYIFGVMII
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NTNVMSPALSAGDGILYYRLTDRYHINDVVVYEVDNTLKVGRERLDSRYYGALPINQI
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/protein_id="AAL96939.1
/db_xref="GI:19747403"
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/protein_id="AAL96938.1"
/db_xref="GI:19747402"
/translation="MKKNKLLLATAILATALGTASLNQNVKAETAGVIDGSTLVVKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HHTKFVAFSTCENFSTDNRVIVVGTIQE"
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6912. .7433
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|Streptococcus pyogenes]"
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|Streptococcus pyogenes]"
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(Streptococcus pyogenes]"
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CTACAGTTTCAAAAACAGGAATAACAAGTGATGAGACACTTGCTTTTGAAAAATAAAG
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                                                                                                           ATTTAAAACATGGGGAAAGTTTAACACTTCAAGGTTTACCAGAAGGTTAATTCTTACCTTG
                                                                                                                                                GTGGAACATATCCGACAAACTCTGGAGAACTCACAGTTACAGATGGAAAAGCTACCTTCA
                                                                                                                                                                                                    GAACTCAGTGGCATCCAGAAGATTTAGTTGGTATTATTCGTATGGAAGATAAAAAAG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGCTGACTTGTTTAGCTATGCTAATAACCCTAGGGCCTCAACAAACGATGAGTTATTAT
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                                        TTACCGAAACGGGTGCTTCAGATTATGAGGTAAGTGTTAATGGAAAAAATGCACCAGATG
                                                                TCAAAGAAACAGATTCTGAAGGCTATAAGGTTAAAGTTAATAGCCAAGAAGTAGCAAATG
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 GGTATTAAGTAAAAACTCAAAAACGATTTACTGTCACTTTAGTGGGAGTCTTTTTAATGAT 110
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sela,S., Aviv,A., Tovi,A., Burstein,I., Caparon,M.G. and Hanski,E. Protein F: an adhesin of Streptococcus pyogenes binds fibronectin via two distinct domains via two distinct domains Microbiol. 10 (5), 1049-1055 (1993)
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   Conservative
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                                                                         /gene="prtf"
/note="repeat domain
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                                                                                                                                                                                                                   LMGGOSESVEFTKDTQTGMSGQTTPQIETEDTKEPEVLMGGQSESVEFTKDTQTGMSG
QTTPQVETEDTKEPEVLMGGQSESVEFTKDTQTGMSGQTTPQIETEDTKEPEVLMGGQ
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                                                                                                                                                       /gene="prtF"
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/strain="JRS75"
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/mol_type="genomic DNA"
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/transl_table=11
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57.2%;
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0; Mismatches
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 Braunschweig,
revised by [4
                           Direct Submission Submitted (31-JUL-1992)
                                                                                                             Streptococcus pyogenes
Streptococcus pyogenes
                                                                                                                                                       S.pyogenes Sfb gene
X67947 S42389
X67947.1 GI:511149
                                                          Talay, S.R.
                                                                                     Streptococcus.
                                                                                                 Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                          fibronectin-binding
                                                                                                                                                                                                                                                                     ACCTGGTGAGACGTCAGAACATAATCCTAAAACTC 1274
                                                                                                                                                                                                                                                                                               TCCAGGAGACCCACCAATGCCTCCAAATCAACCTC 865
                                                                                                                                                                                                                                                                                                                          -- AAAATGAAGCTTACCAAAATCTTTTAAGTGCTGAATATGTACCTGATGATCCCCCTAA 1239
                                                                                                                                                                                                                                                                                                                                                                                  TAATAAAATCCCATCAGGCTATCGTTTAAATATCTTTGAGTCTG
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On Jul 17, 19
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TTATGTAAGAGGGCATCCATATTATAAACAGTTTAGAGTAGCACACGATTTAAGGGTTAA
                                          TGTGCCTCATAGAGTTAGTCAAAATCCT-----
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2 (bases 1 to 1030)
Talay,S.R., Valentin-
Chhatwal,G.S.
Fibronectin-binding p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Talay, S.R., Valentin-Weigand, P., Timmis, K.N. and Chha Domain structure and conserved epitopes of 5tb protein fibronectin-binding adhesin of Streptococcus pyogenes (Microbiol. 13 (3), 531-539 (1994)
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the binding domain involved in
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                                                            TTTGGCATCCGCGGGTGCTATCGGTTTTGGTCAAGTAGCCTATGCTGCCGATGAGAAGAC
                                                                                                     CTTCGCTTTGGTAACTTCCATGGTTGGTGCTAAGACTGTTTTTGGTTTAGTAGAATCCTC
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ALKKLIDFKLSEESLKRVPSTFRLNIESGDKLYQNLYSAETENFRKPETBGP
KTPELDGTPI TEGFORRUSLEPTLPVMLDGOEVPEVSESLEPALPPLMPELDGOE
VPEVPSESLEPALPPLMPELDGOEVPEKPSVDLP IEDPRYEFNKDQSPLAGESGETE
VTEVYGNQQNPVDIDKLPMETGFSCMWYETFDTKEFGVLMGOGSESVEFTKOTQTG
MSGOTTPQVETEDTKEFGVLMGOESVEFTKDTQTGMSGFS
GGQSESVEFTKDTQTGMSGQTTPQVETEDTKEFGVLMGGQSESVEFTKDTQTGMSGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="munkmflukeagflahtkrkrrfavtlygyffmllasagaigfg
Qvayaadektyphrysgupefpwygydfykgfytryhulqlulugsktygaycfulkr
fepkkegsyfpuwykrwdgseetfykyaduprkduessryidveleknilrylyugyp
                                                                                                                                                                                                                                                                                                                                                                         /gene="Sfb"
                                                                                                                                                                                                                                                                                                                                                                                                                       VLPIFSLLKKQTKQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                            ETVTIVEDTRPKLVFHFDNNEPKVEENREKPTKNITPILPATGDIENVLAFLGILILS
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/product="fibronectin-binding
/protein_id="CAA48133.1"
/db_xref="GI:511150"
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/mol_type="genomic DNA"
/strain="DSM 2071"
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Location/Qualifiers
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Pred. No. 5.9e-21;
0; Mismatches 278;
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-GAGTTTCCCTGGTATGGTTATGATTT

290

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AUTHORS
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Kline, J.B., Xu,S., Bisno, A.L. and Collins, C. Identification of a fibronectin-binding prot pathogenic group G streptococci Infect. Immun. 64 (6), 2122-2129 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGU31115 2066 bp DNA linear Group G streptococcus fibronectin binding protein
                                                                                                                            Submitted (06-JUL-1995) James University of Miami, 1600 NW 1 Location/Qualifiers
                                                                                                                                                                  Direct Submission Submitted (06-JUL-
                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus sp. 'group
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U31115
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/gene="gfbA"
252. .1994
                                /db_xref="taxon:1320"
252. .1994
                                                              /mol_type="genomic DNA"
/strain="1750"
                                                                                                organism="Streptococcus
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                   CCGGATGATTTTCAGCTAAGTATTTTTGAGTCTGAGGACAAGGGAGATAAATAT 774
                                                                                               CGTCAAGCTTTGAAGCAACTGATTGATCCGAATTTGGCCAACTAAAATGCCCAAAACAAGTT
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CCTGAGAATTATAAGTTAAATCTTTTTTTTCAAAAGATAACTCGATTCAAAAT
                                                                CGTGATGCTCTTAGAAAATTAATATCACCAGATTTAGAAAAAACAGTCAAAAATCAGTTG
                                                                                                                                GAACAGTGGAAGTCTGAATTAAGAGATGGAGAAATTAGCGAAAGTCAAGTAAAGTTAATG
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EVPEKPS JDLP IEVPRYEPNIKOQSPLAGESGEFEX ITEVETOPWOTDIDKKLEPET
GFSGNNVETEDTKEPEVLMGGGGESVEFTKDTOTGMSGQTTPQVGTEDTKEPGVLMGG
QSESVEFTKDTQTGMSGQTTPQVETEDTKEPGVLMGGQSESVGFTKDTQTGMSGFSET
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DANGIMKGLDRYNAILVTQTAIWYYSDNSKFIVDEQWKSELRDGEISESQVKLMRDAL
RKLISPDLEKTVKNQLPENYKLNLFISKDNSIQNLLSTEYVQDNLQKPGEEPKEESPK
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/trans1_table=11
/product="group G streptococcal
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/db_xref="GI:950169"
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Streptococcus pyogenes
(prtF15) gene, complete
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23, Lund
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes
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                      GACGCCAAACGCAATAAATCCAGATTCAAGTTCGGAATACAGATGGTATGGATATGAATC
                                                                                                         CTTCGCTTTGGTAACTTCCATGGTTGGTGCTAAGACTGTTTTTGGTTTAGTAGAATCCTC
                                                                                                                                                               GGTATTAAGTAAAAACTCAAAACGATTTACTGTCACTTTAGTGGGGGGTCTTTTTAATGAT
       TGAGCCGAATCGTATTA---
                                                                      TTTTGCATGCGCGGGTTCTATCGGTTTTGGTCAAGTAGCCTATGCTGCGGATGAGAAGAC
                                                                                                                                               GGCACACACAAAAAGAAAAGGCGATTTGCTGTCACTTTAGTGGGAGTCTTTTTTATGCT
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VPSESLEPALPPLMPELDGEVPEVPSESLEPALPPLMPELDGEETPEVPSESLEPAL

PPLMPELDGQEVPEKPSIDLPIEVPRYEFNKDQSPLAGESTDYIIFVPSKSLEPAL

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DIDKKLPNETGETSGNAVETEETKEPGYLMGGQSESVEFTKDTQAGMSGQTTPQVETEE

TKEPGYLMGGQSESVEFTKDTQTGMSGQTAPQVETEDTKEPEVLMGGQSESVEFKKDT

QAGMSGQTAPQVETEDTKEPFYLMGGQSESVEFTKDTQTGSSGFSETYSIVEDTRPKL

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NEIMKGIDPLNAILVTQNAIWYYSDSAPINDINNFFTSEANDLNIPPQQLTLMREALR
KLISSDENLVKQVPSNFKLSIFESSDKSYQNLLSAEYVPDDPPKPGDTSEHNPKTPEL
                                                                                                                                                                                                                                                                                                                                          VFHFDNNEPKVEEHREKPTKNITPILPATGDIENVLAFLGILILSVLSIFSLLKNKQN
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/db_xref="GI:2271467"
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/mol_type="genomic DNA"
/strain="EF1949"
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/transl_table=11
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/db_xref="taxon:1314"
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                                 Submitted (23-JUN-1997) Medical Microbiology, Lund University, Solvegatan 23, Lund 22362, Sweden
                                                                      Direct Submission
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Katerov, V.E., Andre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAACGCTATCTTAGTAACACAAAATGCCATATGGTATTACTCGGATAGTGCACCGATTAA 1018
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                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             GI:2267181
                                                                                       Andreev, A.S.,
                                                                                                                                                                                                                                                                                                                                                                                                             321 bp
pyogenes fibronectin
                                                                                                                                                              119-126 (1998)
                                                                                       Schalen, C. and Totolian, A.A.
                                                                                                                                                                                                              and Totolian, A.A.
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binding
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1175

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958 530 901 470 841 410

350

290

BCT 13-FEB-1998 gene, partial

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TITLE
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AF009913
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AUTHORS
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                                                                                            2 (bases 1 to 313)

Katerov,V.E., Andreev,A.S., Schalen,C. and Tol
Direct Submission

Submitted (23-JUN-1997) Medical Microbiology,
                                                                                                                                                                      of the binding region Microbiology 144 (Pt 1), 119-126 (1998)
                                                                                                                                                                                            Katerov, V., Andreev, A., Schalen, C. and Totolian, A.A. Protein F, a fibronectin-binding protein of Streptococcus also binds human fibrinogen: isolation of the protein and fibrinogen:
                                                                                                                                                                                                                                                                      Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                 AF009913
Streptococcus
                                                                                   Solvegatan 23, Lund 22362, Sweden
                                                                                                                                                9467904
                                                                                                                                                                                                                                                  Streptococcus.
                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                               AF009913.1 GI:2267179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTACGGGAGATGAGCTAAATCAGAA 461
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                                                                                                                                                                                                                                   (bases 1 to 313)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
       /organism="Streptococcus pyogenes"
/mol_type="genomic DNA"
/strain="M4 strain 281C"
/db_xref="taxon:1314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"fibronectin binding protein F"
/protein_id="AAC38161.1"
/db_xref="G1:2267182"
/translation="FGQVAYSADEKTVPNFKSDDDDYPWYGYYAYGKGYPGYDISKYY
HDLRYNLNGSQVYQVYCFNIQKIFPYNVKSVTQKWFKKAEGNSDTFGPYAMNPRVQGE
                                                                      Location/Qualifiers
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<1. .>321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Streptococcus pyogenes"
/mol_type="genomic DNA"
/strain="M4 strain Umea"
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Pred. No. 1.3e-06;
0; Mismatches 105
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fibronectin
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AUTHORS
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                                                                                                                                                                                                                                     22354719
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197 CAAGTTCGGAATACAGATGGTATGGATATGAATCTTATGTAAGAGGGCATCCATATTATA
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Mycoplasma penetrans genomic
AP004172 BA000026
AP004172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Infectious Diseases, Department of Bacterial Pathogenesis and Infection Control; 4-7-1 Gakuen, Musashimurayama, Tokyo 208-0011, Japan (F. 1914) Japan (F. 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki, Y.

Direct Submission
Submitted (18-SEP-2001) Yuko Sasaki, National Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The complete genomic sequence of Mycoplasma penetrans, intracellular bacterial pathogen in humans Nucleic Acids Res. 30 (23), 5293-5300 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma penetrans Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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Mycoplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki,Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 293650)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTATTGCTTTAATTTAAAGAAAGCATTTCCTCTCGGATCAGATAGTAGTGTTAAAAAGT 376
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                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="HF-2"
                                                 104.
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/db_xref="taxon:28227"
/gene="MYPE4630"
                                                                                     /note="clinical isolate"
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/transl_table=11
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60.2%;
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Pred. No. 6.6e-06;
0; Mismatches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
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IIEEITKHFNILINGYFRVFLLGTLFNNTKLENGIKNDFKYKKYKSLYWENIVSYIYC
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6048. .
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NKKLFVIY IVWHFHLNLLDTFFFDTETNQSEKNVSKYKNRIIKPLYKBHVLLSIYKFY
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                     TGATGAAGAAACTGAAGGCTATGAATCTGATGATGAAAATGATGAGGAATACTCTGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAGATACCGATCCTGACACTTTCTTAAAACATATCAAAAAAGTAATTGAGAAGGGTTA 1469
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TCCGAATAACAATAACAATCTCTTATTGGAACTCAGTGGCATCCAGAAGATTTAGT 1763
                                                                                                                                                                    CGAATCAGAAGATTCAGAAGAAAACAGTGAAGATGATTCTGAAGAACTTTATGATGAGTC
                                                                                                                                                                                                                          AGACTATCATGGTTTTGGAGACATGAATGATAGTACTTTAGCAG----TTGCTAAAAT 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGTGAAGATGATTCTGAAGAGCTTTATGATGAATCAGATGAAGATAGTG---AATCATA
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                                                                                                           CCTTGTAGAATACGCTCAAGATAGTAATCCTCCACAGCTAACTGACCTTGATTTCTTTAT 1703
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/protein_id="BAC44262.1"
/db_xref="GI:26453932"
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AJ269854, Expect=2.4e-01, Identities=40%"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MPKMKIKKIKESYFINYTNRLEKSSNISKLVSLIESIKKKFTRV/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 293650
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                                                                                                                                                                                                                                                                                                Center code: SC
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Contact: project Information
                                                                                                                                                                Assembly program: XGAPA; version 4.5 Chemistry: Dye-terminator; 100% of reads Consensus quality: 144211 bases at least Consensus quality: 14460 bases at least Consensus quality: 144678 bases at least
                                                                                                      Insert size: 145065; sum-of-contigs
Insert size: 156629; 0.9% error; agarose-fp
Quality coverage: 8.29x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                        Center project name: zC266K22
------ Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 5, 2003 this sequence version replaced gi:28949357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 145265)
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL935272 145265 bp
Danio rerio clone CH211-266K22,
                                                                                    coverage: 7.97x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andrew, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unordered pieces.
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
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Best Local Similarity 43.3%;
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                                                                                                                                                                                                                                                                                     TACTTTAGCAGTTGCTAAAATCCTTGTAGAATACGCTCAAGATAGTAATCCTCCACAGCT 1682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                AGATTTCCATTTTGAAATTGAATTAAAAAATAATAAGCAAGAATTGCTTTCTCAAACTGT 1922
                                                 TGTAACTCATAATTTAACATTGAGAAAAACGGTGACTGGTTTAGCTGGTGACAGAACTAA 1862
                                                                                                                       GTGGCATCCAGAAGATTTAGTTGATATTATTCGTATGGAAGATAAAAAAGAAGTTATACC 1802
                                                                                                                                                                                             AACTGACCTTGATTTCTTTATTCCGAATAACAATAATATCAATCTCTTATTGGAACTCA 1742
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fragment_chain:1"
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-266K22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'clone_lib="CHORI-211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97678: contig of 97678 bp in length
97778: gap of 100 bp
101129: contig of 3351 bp in length
101229: gap of 100 bp
145265: contig of 44036 bp in length
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                                                                                                     TGGGGAAAGTTTAACACTTCAAGGTTTACCAGAAGGTTATTCTTACCTTGTCAAAGAAAC
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Search completed: August 19, 2003, 12:03:45 Job time: 8158 secs